

Figures

Figure 1 - Nucleotide and protein sequence of *Aspergillus ochraceus* 11 alpha hydroxylase

5	tggaagtttt tacacttatt atgccggagc cgaagattc tgagtcgagg ggttggggaa	60
	caacactata agacctataa ccacttggat ttggtgaatt tacacgggca ttatcaaaac	120
	agccacaagc tgacagctca ttatc atg ccc ttc ttc act ggg ctt ctg gcg	172
	Met Pro Phe Phe Thr Gly Leu Leu Ala	
	1 5	
10	att tac cat agt ctc ata ctc gac aac cca gtc caa acc ctg agc acc	220
	Ile Tyr His Ser Leu Ile Leu Asp Asn Pro Val Gln Thr Leu Ser Thr	
	10 15 20 25	
15	att gtc gta ttg gcg gca gcg tac tgg ctc gca acg ctc cag ccg agc	268
	Ile Val Val Leu Ala Ala Ala Tyr Trp Leu Ala Thr Leu Gln Pro Ser	
	30 35 40	
20	gac ctt cct gag ctg aat ccc gcc aaa cca ttc gag ttc acc aat cgt	316
	Asp Leu Pro Glu Leu Asn Pro Ala Lys Pro Phe Glu Phe Thr Asn Arg	
	45 50 55	
25	cgt cgt gtt cat gag ttt gtt gaa aat agt aag agc ttg ctt gct cgg	364
	Arg Arg Val His Glu Phe Val Glu Asn Ser Lys Ser Leu Leu Ala Arg	
	60 65 70	
30	ggg agg gaa ttg cac ggg cac gag ccg tac aga ctc atg tct gaa tgg	412
	Gly Arg Glu Leu His Gly His Glu Pro Tyr Arg Leu Met Ser Glu Trp	
	75 80 85	
35	gga tcc ttg att gtc ctg ccc cca gag tgc gcc gac gag ctg cgc aac	460
	Gly Ser Leu Ile Val Leu Pro Pro Glu Cys Ala Asp Glu Leu Arg Asn	
	90 95 100 105	
40	gac cca aga atg gac ttt gag acg ccc acc acc gac gac tcc cac gga	508
	Asp Pro Arg Met Asp Phe Glu Thr Pro Thr Thr Asp Asp Ser His Gly	
	110 115 120	
45	tat atc cct ggc ttc gac gct ctc aac gca gac ccg aac ctg act aaa	556
	Tyr Ile Pro Gly Phe Asp Ala Leu Asn Ala Asp Pro Asn Leu Thr Lys	
	125 130 135	
50	gtg gtc acc aag tac ctc aca aaa gca ttg aac aag ctt act gct ccg	604
	Val Val Thr Lys Tyr Leu Thr Lys Ala Leu Asn Lys Leu Thr Ala Pro	
	140 145 150	
55	atc tcg cat gaa gcg tcc atc gcc atg aaa gcg gtg ctg ggt gac gat	652
	Ile Ser His Glu Ala Ser Ile Ala Met Lys Ala Val Leu Gly Asp Asp	
	155 160 165	
60	cca gat tgg cgt gag atc tac cca gcc aga gac ttg ctc cag ctc gtc	700
	Pro Asp Trp Arg Glu Ile Tyr Pro Ala Arg Asp Leu Leu Gln Leu Val	
	170 175 180 185	
65	gcc cgg atg tcg aca aga gtg ttc ctt ggc gag gaa atg tgc aat aac	748
	Ala Arg Met Ser Thr Arg Val Phe Leu Gly Glu Glu Met Cys Asn Asn	
	190 195 200	
70	cag gat tgg atc caa acc tca tca caa tac gcg gcc ctt gcc ttc ggt	796
	Gln Asp Trp Ile Gln Thr Ser Ser Gln Tyr Ala Ala Leu Ala Phe Gly	
	205 210 215	
75	gtc ggt gac aag ctt aga ata tac ccg aga atg atc aga ccg ata gta	844
	Val Gly Asp Lys Leu Arg Ile Tyr Pro Arg Met Ile Arg Pro Ile Val	
	220 225 230	
80	cat tgg ttc atg cca tcc tgt tgg gag ctg cgc cga tcg ctg cga cgc	892
	His Trp Phe Met Pro Ser Cys Trp Glu Leu Arg Arg Ser Leu Arg Arg	
	235 240 245	
85	tgc cga cag att ctc acg ccg tac att cac aaa cgc aag tcc ctg aag	940
	Cys Arg Gln Ile Leu Thr Pro Tyr Ile His Lys Arg Lys Ser Leu Lys	
	250 255 260 265	
90	ggg acc acg gac gag cag gcc aag ccc ctt atg ttt gat gat tcc atc	988
	Gly Thr Thr Asp Glu Gln Gly Lys Pro Leu Met Phe Asp Asp Ser Ile	
	270 275 280	

5	gag tgg ttc gag cga gag ctg ggt ccc aac cac gac gcg gtc ctg aag Glu Trp Phe Glu Arg Glu Leu Gly Pro Asn His Asp Ala Val Leu Lys 285 290 295	1036
10	cag gtc acg ctc tcc ata gtt gct atc cac acc acg agt gac cta ctc Gln Val Thr Leu Ser Ile Val Ala Ile His Thr Thr Ser Asp Leu Leu 300 305 310	1084
15	ttg cag gcc atg agc gat ctc gcg cag aac ccg aaa gtg cta caa gca Leu Gln Ala Met Ser Asp Leu Ala Gln Asn Pro Lys Val Leu Gln Ala 315 320 325	1132
20	gtg cgc gag gag gtg gtc cga gtg ctg agc acc gag ggg ctc agc aag Val Arg Glu Glu Val Val Arg Val Leu Ser Thr Glu Gly Leu Ser Lys 330 335 340 345	1180
25	gtc tcg ctt cac agt ctc aag ctc atg gac agc gcg ttg aag gaa agc Val Ser Leu His Ser Leu Lys Leu Met Asp Ser Ala Leu Lys Glu Ser 350 355 360	1228
30	cag cgt ctc agg cct acg ctt ctc ggc tcc ttt cgt cgg cag gca acg Gln Arg Leu Arg Pro Thr Leu Leu Gly Ser Phe Arg Arg Gln Ala Thr 365 370 375	1276
35	aat gac atc aag ctg aag agc ggg ttt gtc ata aag aaa ggg act aga Asn Asp Ile Lys Leu Lys Ser Gly Phe Val Ile Lys Lys Gly Thr Arg 380 385 390	1324
40	gtc gtg atc gac agc acc cat atg tgg aat ccc gag tat tac act gac Val Val Ile Asp Ser Thr His Met Trp Asn Pro Glu Tyr Tyr Thr Asp 395 400 405	1372
45	cct ctc cag tac gac ggg tac cgc tac ttc aac aag cgg cag aca ccc Pro Leu Gln Tyr Asp Gly Tyr Arg Tyr Phe Asn Lys Arg Gln Thr Pro 410 415 420 425	1420
50	ggc gag gac aag aac gcg ttg ctc gtc agc aca agc gcc aac cac atg Gly Glu Asp Lys Asn Ala Leu Leu Val Ser Thr Ser Ala Asn His Met 430 435 440	1468
55	gga ttc ggt cac ggc gtt cac gcc tgt cct ggc aga ttc ttc gcc tcc Gly Phe Gly His Gly Val His Ala Cys Pro Gly Arg Phe Phe Ala Ser 445 450 455	1516
60	aac gag atc aag att gcc ttg tgt cat atc atc tta aat tat gag tgg Asn Glu Ile Lys Ile Ala Leu Cys His Ile Ile Leu Asn Tyr Glu Trp 460 465 470	1564
65	cgt ctt cca gac ggc ttc aag ccc cag cct ctc aac atc ggg atg act Arg Leu Pro Asp Gly Phe Lys Pro Gln Pro Leu Asn Ile Gly Met Thr 475 480 485	1612
70	tat ctg gcg gat ccc aat acc agg atg ctg atc agg cca cgc aag gcg Tyr Leu Ala Asp Pro Asn Thr Arg Met Leu Ile Arg Pro Arg Lys Ala 490 495 500 505	1660
75	gag atc gat atg gcg agt tta act gtg tag gtcgaacacg aagtcctgat Glu Ile Asp Met Ala Ser Leu Thr Val *	1710
80	gaagtgttat tggtcagtgg gtgaagcaag tcgcagaaat gtgtaacaat ttataagaat aaaaaa	1770 1776

**Figure 2 - Nucleotide and protein sequence of human
oxidoreductase**

5	atg gga gac tcc cac gtg gac acc agc tcc acc gtg tcc gag gcg gtg Met Gly Asp Ser His Val Asp Thr Ser Thr Val Ser Glu Ala Val	48
10	gcc gaa gaa gta tct ctt ttc agc atg acg gac atg att ctg ttt tcg Ala Glu Glu Val Ser Leu Phe Ser Met Thr Asp Met Ile Leu Phe Ser	96
15	ctc atc gtg ggt ctc cta acc tac tgg ttc ctc ttc aga aag aaa aaa Leu Ile Val Gly Leu Leu Thr Tyr Trp Phe Leu Phe Arg Lys Lys Lys	144
20	gaa gaa gtc ccc gag ttc acc aaa att cag aca ttg acc tcc tct gtc Glu Glu Val Pro Glu Phe Thr Lys Ile Gln Thr Leu Thr Ser Ser Val	192
25	aga gag agc agc ttt gtg gaa aag atg aag aaa acg ggg agg aac atc Arg Glu Ser Ser Phe Val Glu Lys Met Lys Lys Thr Gly Arg Asn Ile	240
30	atc gtg ttc tac ggc tcc cag acg ggg act gca gag gag ttt gcc aac Ile Val Phe Tyr Gly Ser Gln Thr Gly Thr Ala Glu Glu Phe Ala Asn	288
35	cgc ctg tcc aag gac gcc cac cgc tac ggg atg cga ggc atg tca gcg Arg Leu Ser Lys Asp Ala His Arg Tyr Gly Met Arg Gly Met Ser Ala	336
40	gac cct gag gag tat gac ctg gcc gac ctg agc agc ctg cca gag atc Asp Pro Glu Glu Tyr Asp Leu Ala Asp Leu Ser Ser Leu Pro Glu Ile	384
45	gac aac gcc ctg gtg gtt ttc tgc atg gcc acc tac ggt gag gga gac Asp Asn Ala Leu Val Val Phe Cys Met Ala Thr Tyr Gly Glu Gly Asp	432
50	ccc acc gac aat gcc cag gac ttc tac gac tgg ctg cag gag aca gac Pro Thr Asp Asn Ala Gln Asp Phe Tyr Asp Trp Leu Gln Glu Thr Asp	480
55	gtg gat ctc tct ggg gtc aag ttc gcg gtg ttt ggt ctt ggg aac aag Val Asp Leu Ser Gly Val Lys Phe Ala Val Phe Gly Leu Gly Asn Lys	528
60	acc tac gag cac ttc aat gcc atg ggc aag tac gtg gac aag cgg ctg Thr Tyr Glu His Phe Asn Ala Met Gly Lys Tyr Val Asp Lys Arg Leu	576
65	gag cag ctc ggc gcc cag cgc atc ttt gag ctg ggg ttg ggc gac gac Glu Gln Leu Gly Ala Gln Arg Ile Phe Glu Leu Gly Leu Gly Asp Asp	624
70	gat ggg aac ttg gag gag gac ttc atc acc tgg cga gag cag ttc tgg Asp Gly Asn Leu Glu Glu Asp Phe Ile Thr Trp Arg Glu Gln Phe Trp	672
75	cag gcc gtg tgt gaa cac ttt ggg gtg gaa gcc act ggc gag gag tcc Pro Ala Val Cys Glu His Phe Gly Val Glu Ala Thr Gly Glu Glu Ser	720
80	agc att cgc cag tac gag ctt gtg gtc cac acc gac ata gat gcg gcc Ser Ile Arg Gln Tyr Glu Leu Val Val His Thr Asp Ile Asp Ala Ala	768
85	aag gtg tac atg ggg gag atg ggc cgg ctg aag agc tac gag aac cag Lys Val Tyr Met Gly Glu Met Gly Arg Leu Lys Ser Tyr Glu Asn Gln	816
90	aag ccc ccc ttt gat gcc aag aat cgg ttc ctg gct gca gtc acc acc Lys Pro Pro Phe Asp Ala Lys Asn Pro Phe Leu Ala Ala Val Thr Thr	864
95	aac cgg aag ctg aac cag gga acc gag cgc cac ctc atg cac ctg gaa Asn Arg Lys Leu Asn Gln Gly Thr Glu Arg His Leu Met His Leu Glu	912
100	ttg gac atc tcg gac tcc aaa atc agg tat gaa tct ggg gac cac gtg Leu Asp Ile Ser Asp Ser Lys Ile Arg Tyr Glu Ser Gly Asp His Val	960

	305	310	315	320	
5	gct gtg tac cca gcc aac gac tct gct ctc gtc aac cag ctg ggc aaa Ala Val Tyr Pro Ala Asn Asp Ser Ala Leu Val Asn Gln Leu Gly Lys 325 330 335	1008			
10	atc ctg ggt gcc gac ctg gac gtc gtc atg tcc ctg aac aac ctg gat Ile Leu Gly Ala Asp Leu Asp Val Val Met Ser Leu Asn Asn Leu Asp 340 345 350	1056			
15	gag gag tcc aac aag aag cac cca ttc ccg tgc cct acg tcc tac cgc Glu Glu Ser Asn Lys Lys His Pro Phe Pro Cys Pro Thr Ser Tyr Arg 355 360 365	1104			
20	acg gcc ctc acc tac tac ctg gac atc acc aac ccg ccg cgt acc aac Thr Ala Leu Thr Tyr Tyr Leu Asp Ile Thr Asn Pro Pro Arg Thr Asn 370 375 380	1152			
25	gtg ctg tac gag ctg gcg cag tac gcc tcg gag ccc tcg gag cag gag Val Leu Tyr Glu Leu Ala Gln Tyr Ala Ser Glu Pro Ser Glu Gln Glu 385 390 400	1200			
30	ctg ctg cgc aag atg gcc tcc tcc tcc ggc gag ggc aag gag ctg tac Leu Leu Arg Lys Met Ala Ser Ser Ser Gly Glu Gly Lys Glu Leu Tyr 405 410 415	1248			
35	ctg agc tgg gtg gtg gag gcc ccg agg cac atc ctg gcc atc ctg cag Leu Ser Trp Val Val Glu Ala Arg Arg His Ile Leu Ala Ile Leu Gln 420 425 430	1296			
40	gac tgc ccg tcc ctg ccg ccc ccc atc gac cac ctg tgt gag ctg ctg Asp Cys Pro Ser Leu Arg Pro Pro Ile Asp His Leu Cys Glu Leu Leu 435 440 445	1344			
45	ccg cgc ctg cag gcc cgc tac tac tcc atc gcc tca tcc tcc aag gtc Pro Arg Leu Gln Ala Arg Tyr Tyr Ser Ile Ala Ser Ser Ser Lys Val 450 455 460	1392			
50	cac ccc aac tct gtg cac atc tgt gcg gtg gtt gtg gag tac gag acc His Pro Asn Ser Val His Ile Cys Ala Val Val Val Glu Tyr Glu Thr 465 470 475 480	1440			
55	aag gcc ggc cgc atc aac aag ggc gtg gcc acc aac tgg ctg cgc gcc Lys Ala Gly Arg Ile Asn Lys Gly Val Ala Thr Asn Trp Leu Arg Ala 485 490 495	1488			
60	aag gag cct gcc ggg gag aac ggc ggc cgt gcg ctg gtg ccc atg ttc Lys Glu Pro Ala Gly Glu Asn Gly Arg Ala Leu Val Pro Met Phe 500 505 510	1536			
65	gtg cgc aag tcc cag ttc cgc ctg ccc ttc aag gcc acc acg cct gtc Val Arg Lys Ser Gln Phe Arg Leu Pro Phe Lys Ala Thr Thr Pro Val 515 520 525	1584			
70	atc atg gtg ggc ccc ggc acc ggg gtg gca ccc ttc ata ggc ttc atc Ile Met Val Gly Pro Gly Thr Gly Val Ala Pro Phe Ile Gly Phe Ile 530 535 540	1632			
75	cag gag cgc gcc tgg ctg cga cag cag ggc aag gag gtg ggg gag acg Gln Glu Arg Ala Trp Leu Arg Gln Gln Gly Lys Glu Val Gly Glu Thr 545 550 555 560	1680			
80	ctg ctg tac tac ggc tgc cgc cgc tcg gat gag gac tac ctg tac cgc Leu Leu Tyr Tyr Gly Cys Arg Arg Ser Asp Glu Asp Tyr Leu Tyr Arg 565 570 575	1728			
85	gag gag ctg gcg cag ttc cac agg gac ggt gcg ctc acc cag ctc aac Glu Glu Leu Ala Gln Phe His Arg Asp Gly Ala Leu Thr Gln Leu Asn 580 585 590	1776			
	gtg gcc ttc tcc ccg gag cag tcc cac aag gtc tac gtc cag cac ctg Val Ala Phe Ser Arg Glu Gln Ser His Lys Val Tyr Val Gln His Leu 595 600 605	1824			
	cta aag caa gac cga gag cac ctg tgg aag ttg atc gaa ggc ggt gcc Leu Lys Gln Asp Arg Glu His Leu Trp Lys Leu Ile Glu Gly Gly Ala 610 615 620	1872			
	cac atc tac gtc tgt ggg gat gca ccg aac atg gcc agg gat gtg cag His Ile Tyr Val Cys Gly Asp Ala Arg Asn Met Ala Arg Asp Val Gln 625 630 635 640	1920			
	aac acc ttc tac gac atc gtg gct gag ctc ggg gcc atg gag cac gcg Asn Thr Phe Tyr Asp Ile Val Ala Glu Leu Gly Ala Met Glu His Ala 645 650 655	1968			

[illegible]

5

Figure 3 - Nucleotide and protein sequence of *Aspergillus ochraceus oxidoreductase*

5	cttatttcgt ttaggaagag caccggcttc ggtgtccttc cttaccctct tattcttcct cttctgactc cctttttgtt attgatcgcc catctcggtg aacatttggg atatctttcc ctctccccct cccgccccga cctctcttat cttctctccc cgtccagcat ttagctcgcc atcgaaattcg caattccttc ctcgtgactc ttcacgtctg agcgtcctca tc atg gcg Met Ala 1	60 120 180 238
10	caa ctc gat act ctc gat ttg gtc gtc ctg gtg gcg ctc ttg gtg ggt Gln Leu Asp Thr Leu Asp Leu Val Val Leu Val Ala Leu Leu Val Gly 5 10 15	286
15	agc gtg gcc tac ttc acc aag ggc acc tac tgg gcc gtc gcc aaa gac Ser Val Ala Tyr Phe Thr Lys Gly Thr Tyr Trp Ala Val Ala Lys Asp 20 25 30	334
20	cct tat gcc tcg gct ggt ccg gcg atg aat gga ggc gcc aag gcc ggc Pro Tyr Ala Ser Ala Gly Pro Ala Met Asn Gly Gly Ala Lys Ala Gly 35 40 45 50	382
25	aag act cgc gac att gtt cag aaa atg gac gaa act ggc aaa aac tgt Lys Thr Arg Asp Ile Val Gln Lys Met Asp Glu Thr Gly Lys Asn Cys 55 60 65	430
30	gtg att ttc tac ggc tcg caa acc ggt acc gct gag gac tac gcg tcc Val Ile Phe Tyr Gly Ser Gln Thr Gly Thr Ala Glu Asp Tyr Ala Ser 70 75 80	478
35	aga ctg gcc aag gaa ggc tcc cag cga ttc ggt ctc aag acc atg gtg Arg Leu Ala Lys Glu Gly Ser Gln Arg Phe Gly Leu Lys Thr Met Val 85 90 95	526
40	gcc gat ctg gag gac tac gac tac gaa aac ctg gaa aag ttc ccc gag Ala Asp Leu Glu Asp Tyr Asp Tyr Glu Asn Leu Glu Lys Phe Pro Glu 100 105 110	574
45	gac aag gtt gtt ttc ttc gtt ctg gcc act tat ggc gag ggt gaa ccc Asp Lys Val Val Phe Phe Val Leu Ala Thr Tyr Gly Glu Gly Glu Pro 115 120 125 130	622
50	acg gat aat cgc gtt gaa ttc tac cag ttc gtc acg ggc gaa gat gct Thr Asp Asn Ala Val Glu Phe Tyr Gln Phe Val Thr Gly Glu Asp Ala 135 140 145	670
55	gct ttc gag agc ggc gct acc gcc gac gat aag cct ctg tct tct ctc Ala Phe Glu Ser Gly Ala Thr Ala Asp Asp Lys Pro Leu Ser Ser Leu 150 155 160	718
60	aag tat gtc acg ttt ggt ctg ggt aac aac acc tat gag cac tac aac Lys Tyr Val Thr Phe Gly Leu Gly Asn Asn Thr Tyr Glu His Tyr Asn 165 170 175	766
65	gct atg gtt cgc aat gtg gac gcc gct ctc aca aag ttc ggc gcc caa Ala Met Val Arg Asn Val Asp Ala Ala Leu Thr Lys Phe Gly Ala Gln 180 185 190	814
70	cgc att ggc tct gct ggt gag ggt gac gac ggc gct ggt aca atg gaa Arg Ile Gly Ser Ala Gly Glu Gly Asp Asp Gly Ala Gly Thr Met Glu 195 200 205 210	862
75	gag gat ttc ctg gcc tgg aag gaa ccc atg tgg gct gcc ctt tct gag Glu Asp Phe Leu Ala Trp Lys Glu Pro Met Trp Ala Ala Leu Ser Glu 215 220 225	910
80	gcg atg aac ctg caa gag cgc gat gcg gtc tac gag ccg gtc ttc aat Ala Met Asn Leu Gln Glu Arg Asp Ala Val Tyr Glu Pro Val Phe Asn 230 235 240	958
85	gtc acc gag gac gag tcc ctg agc ccc gaa gat gag aac gtt tac ctc Val Thr Glu Asp Glu Ser Leu Ser Pro Glu Asp Glu Asn Val Tyr Leu 245 250 255	1006
90	ggt gag ccc act caa ggt cat ctc caa ggc gag ccc aag ggc ccg tac Gly Glu Pro Thr Gln Gly His Leu Gln Gly Glu Pro Lys Gly Pro Tyr 260 265 270	1054
95	tct gcg cac aac ccg ttc atc gct ccc atc tcc gaa tct cgt gaa ctg Ser Ala His Asn Pro Phe Ile Ala Pro Ile Ser Glu Ser Arg Glu Leu 275 280 285 290	1102

5	ttc aac gtc aag gac cgc aac tgt ctg cac atg gaa atc agc atc gcc Phe Asn Val Lys Asp Arg Asn Cys Leu His Met Glu Ile Ser Ile Ala 295 300 305	1150
10	ggg agc aac ctc act tac cag act ggt gac cac atc gct gtt tgg ccc Gly Ser Asn Leu Thr Tyr Gln Thr Gly Asp His Ile Ala Val Trp Pro 310 315 320	1198
15	acc aac gcc ggt tcc gag gtc gat cgg ttc ctg cag gct ttt ggt ctc Thr Asn Ala Gly Ser Glu Val Asp Arg Phe Leu Gln Ala Phe Gly Leu 325 330 335	1246
20	gaa gga aag cgc cac tcc gtc atc aac att aag ggt atc gat gtg acc Glu Gly Lys Arg His Ser Val Ile Asn Ile Lys Gly Ile Asp Val Thr 340 345 350	1294
25	gct aag gtt ccg att ccc act cct acg acc tat gac gcc gca gtt cgc Ala Lys Val Pro Ile Pro Thr Pro Thr Tyr Asp Ala Ala Val Arg 355 360 365 370	1342
30	tac tac ctg gaa gtc tgt gcc ccc gtt tcc cgt cag ttt gtc tgc act Tyr Tyr Leu Glu Val Cys Ala Pro Val Ser Arg Gln Phe Val Ser Thr 375 380 385	1390
35	ctc gct gcc ttt gcc cct gat gaa gcg acc aag gcg gag atc gtt cgt Leu Ala Ala Phe Ala Pro Asp Glu Ala Thr Lys Ala Glu Ile Val Arg 390 395 400	1438
40	ttg ggt ggc gac aag gac tat ttc cat gag aag att acc aac cga tgc Leu Gly Gly Asp Lys Asp Tyr Phe His Glu Lys Ile Thr Asn Arg Cys 405 410 415	1486
45	ttc aac atc gct cag gct ctc cag agc atc acg tcc aag cct ttc acc Phe Asn Ile Ala Gln Ala Leu Gln Ser Ile Thr Ser Lys Pro Phe Thr 420 425 430	1534
50	gcc gtc ccg ttc tcc ctg ctt atc gaa ggt atc acc aag ctt cag ccc Ala Val Pro Phe Ser Leu Leu Ile Glu Gly Ile Thr Lys Leu Gln Pro 435 440 445 450	1582
55	cgt tac tac tcg atc tcc tcg tct tcc ctg gtt cag aag gac aag att Arg Tyr Tyr Ser Ile Ser Ser Ser Ser Leu Val Gln Lys Asp Lys Ile 455 460 465	1630
60	agc att acc gcc gtt gtg gag tcg gtt cgc ttg cct ggt gag gaa cac Ser Ile Thr Ala Val Val Glu Ser Val Arg Leu Pro Gly Glu Glu His 470 475 480	1678
65	att gtc aag ggt gtg acc acg aac tat ctt ctc gcg ctc aag gaa aag Ile Val Lys Gly Val Thr Thr Asn Tyr Leu Leu Ala Leu Lys Glu Lys 485 490 495	1726
70	caa aac ggc gag cct tcc cct gac ccg cac ggc ttg act tac tct atc Gln Asn Gly Glu Pro Ser Pro Asp Pro His Gly Leu Thr Tyr Ser Ile 500 505 510	1774
75	act gga ccc cgt aac aag tac gat ggc atc cat gtc ccc gtt cac gtc Thr Gly Pro Arg Asn Lys Tyr Asp Gly Ile His Val Pro Val His Val 515 520 525 530	1822
80	cgc cac tcg aac ttc aaa ttg ccc tcg gat ccc tcg cga cct gtg atc Arg His Ser Asn Phe Lys Leu Pro Ser Asp Pro Ser Arg Pro Val Ile 535 540 545	1870
85	atg gtt gga ccc ggt act ggt gtt gct cct ttc cgt ggg ttt atc cag Met Val Gly Pro Gly Thr Gly Val Ala Pro Phe Arg Gly Phe Ile Gln 550 555 560	1918
90	gag cgt gct gcc ttg gcc gcg aag ggc gag aag gtc gga act acc ttg Glu Arg Ala Ala Leu Ala Ala Lys Gly Glu Lys Val Gly Thr Thr Leu 565 570 575	1966
95	ctt ttc ttc ggc tgc cgt aag tcc gac gaa gat ttc ttg tac aag gat Leu Phe Phe Gly Cys Arg Lys Ser Asp Glu Asp Phe Leu Tyr Lys Asp 580 585 590	2014
100	gaa tgg aag act ttt cag gag cag ctt ggc gac tcg ctc aag atc atc Glu Trp Lys Thr Phe Gln Glu Gln Leu Gly Asp Ser Leu Lys Ile Ile 595 600 605 610	2062
105	act gcc ttc tct cgt gaa tcg gct gag aaa gtc tac gtc cag cac agg Thr Ala Phe Ser Arg Glu Ser Ala Glu Lys Val Tyr Val Gln His Arg 615 620 625	2110
110	ctg cgt gag cat gcc gag ctg gtc agt gac ctg ctg aag cag aaa gcc	2158

	Leu	Arg	Glu	His	Ala	Glu	Leu	Val	Ser	Asp	Leu	Leu	Lys	Gln	Lys	Ala	
				630					635					640			
5	act	ttc	tat	gtt	tgc	ggt	gac	gct	gcc	aac	atg	gcc	cgt	gaa	gtc	aac	2206
	Thr	Phe	Tyr	Val	Cys	Gly	Asp	Ala	Ala	Asn	Met	Ala	Arg	Glu	Val	Asn	
			645					650					655				
	ctc	gtg	ctt	ggg	caa	atc	att	gcc	aag	cag	cgc	ggt	ctc	cct	gcc	gag	2254
10	Leu	Val	Leu	Gly	Gln	Ile	Ile	Ala	Lys	Gln	Arg	Gly	Leu	Pro	Ala	Glu	
			660				665					670					
	aag	ggc	gag	gag	atg	gtg	aag	cac	atg	cgc	agc	agc	ggc	agc	tac	cag	2302
	Lys	Gly	Glu	Glu	Met	Val	Lys	His	Met	Arg	Ser	Ser	Gly	Ser	Tyr	Gln	
						680					685					690	
15	gac	gat	gtc	tgg	tcc	taa	aa										2322
	Asp	Asp	Val	Trp	Ser	*											
					695												

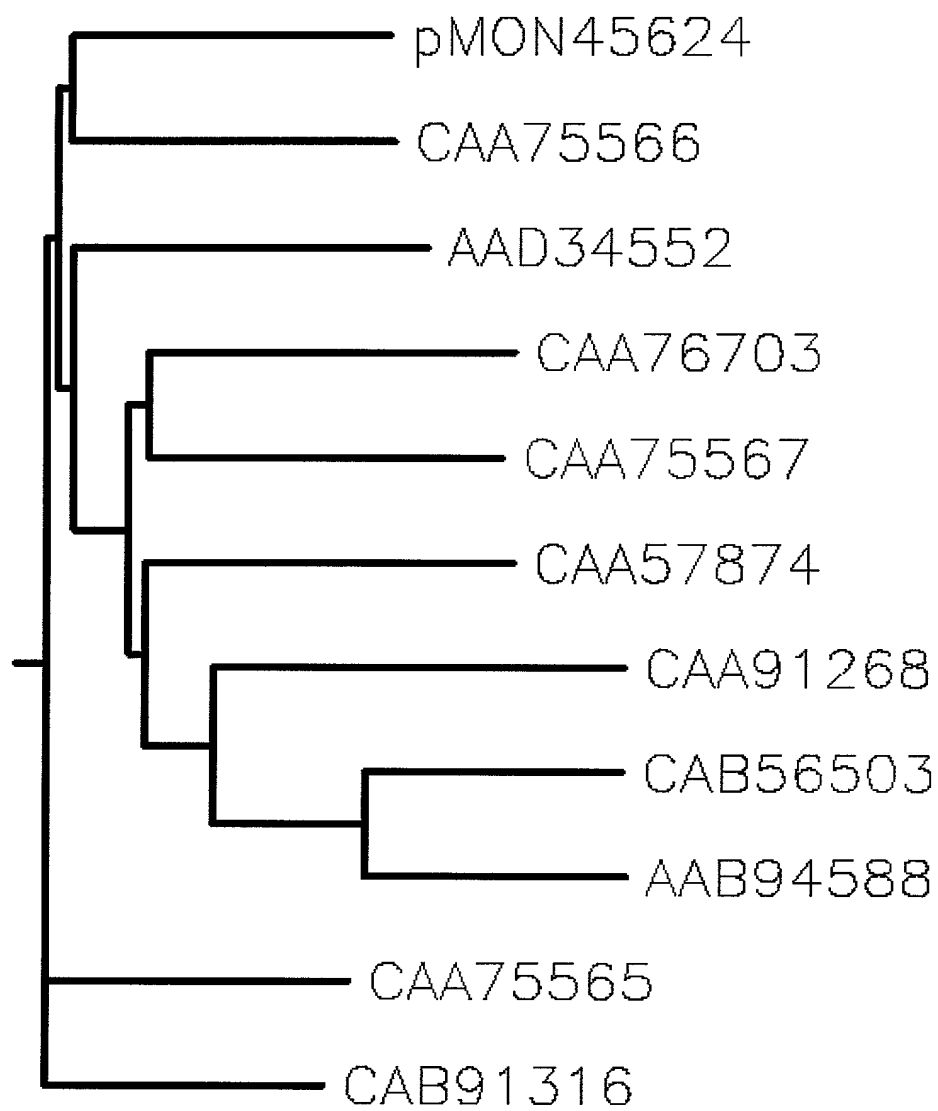
1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60
61
62
63
64
65
66
67
68
69
70
71
72
73
74
75
76
77
78
79
80
81
82
83
84
85
86
87
88
89
90
91
92
93
94
95
96
97
98
99
100
101
102
103
104
105
106
107
108
109
110
111
112
113
114
115
116
117
118
119
120
121
122
123
124
125
126
127
128
129
130
131
132
133
134
135
136
137
138
139
140
141
142
143
144
145
146
147
148
149
150
151
152
153
154
155
156
157
158
159
160
161
162
163
164
165
166
167
168
169
170
171
172
173
174
175
176
177
178
179
180
181
182
183
184
185
186
187
188
189
190
191
192
193
194
195
196
197
198
199
200
201
202
203
204
205
206
207
208
209
210
211
212
213
214
215
216
217
218
219
220
221
222
223
224
225
226
227
228
229
230
231
232
233
234
235
236
237
238
239
240
241
242
243
244
245
246
247
248
249
250
251
252
253
254
255
256
257
258
259
260
261
262
263
264
265
266
267
268
269
270
271
272
273
274
275
276
277
278
279
280
281
282
283
284
285
286
287
288
289
290
291
292
293
294
295
296
297
298
299
300
301
302
303
304
305
306
307
308
309
310
311
312
313
314
315
316
317
318
319
320
321
322
323
324
325
326
327
328
329
330
331
332
333
334
335
336
337
338
339
340
341
342
343
344
345
346
347
348
349
350
351
352
353
354
355
356
357
358
359
360
361
362
363
364
365
366
367
368
369
370
371
372
373
374
375
376
377
378
379
380
381
382
383
384
385
386
387
388
389
390
391
392
393
394
395
396
397
398
399
400
401
402
403
404
405
406
407
408
409
410
411
412
413
414
415
416
417
418
419
420
421
422
423
424
425
426
427
428
429
430
431
432
433
434
435
436
437
438
439
440
441
442
443
444
445
446
447
448
449
450
451
452
453
454
455
456
457
458
459
460
461
462
463
464
465
466
467
468
469
470
471
472
473
474
475
476
477
478
479
480
481
482
483
484
485
486
487
488
489
490
491
492
493
494
495
496
497
498
499
500
501
502
503
504
505
506
507
508
509
510
511
512
513
514
515
516
517
518
519
520
521
522
523
524
525
526
527
528
529
530
531
532
533
534
535
536
537
538
539
540
541
542
543
544
545
546
547
548
549
550
551
552
553
554
555
556
557
558
559
560
561
562
563
564
565
566
567
568
569
570
571
572
573
574
575
576
577
578
579
580
581
582
583
584
585
586
587
588
589
590
591
592
593
594
595
596
597
598
599
600
601
602
603
604
605
606
607
608
609
610
611
612
613
614
615
616
617
618
619
620
621
622
623
624
625
626
627
628
629
630
631
632
633
634
635
636
637
638
639
640
641
642
643
644
645
646
647
648
649
650
651
652
653
654
655
656
657
658
659
660
661
662
663
664
665
666
667
668
669
670
671
672
673
674
675
676
677
678
679
680
681
682
683
684
685
686
687
688
689
690
691
692
693
694
695
696
697
698
699
700
701
702
703
704
705
706
707
708
709
710
711
712
713
714
715
716
717
718
719
720
721
722
723
724
725
726
727
728
729
730
731
732
733
734
735
736
737
738
739
740
741
742
743
744
745
746
747
748
749
750
751
752
753
754
755
756
757
758
759
760
761
762
763
764
765
766
767
768
769
770
771
772
773
774
775
776
777
778
779
780
781
782
783
784
785
786
787
788
789
790
791
792
793
794
795
796
797
798
799
800
801
802
803
804
805
806
807
808
809
810
811
812
813
814
815
816
817
818
819
820
821
822
823
824
825
826
827
828
829
830
831
832
833
834
835
836
837
838
839
840
841
842
843
844
845
846
847
848
849
850
851
852
853
854
855
856
857
858
859
860
861
862
863
864
865
866
867
868
869
870
871
872
873
874
875
876
877
878
879
880
881
882
883
884
885
886
887
888
889
890
891
892
893
894
895
896
897
898
899
900
901
902
903
904
905
906
907
908
909
910
911
912
913
914
915
916
917
918
919
920
921
922
923
924
925
926
927
928
929
930
931
932
933
934
935
936
937
938
939
940
941
942
943
944
945
946
947
948
949
950
951
952
953
954
955
956
957
958
959
960
961
962
963
964
965
966
967
968
969
970
971
972
973
974
975
976
977
978
979
980
981
982
983
984
985
986
987
988
989
990
991
992
993
994
995
996
997
998
999
1000

Figure 4 - Amino acid homology alignment of *A. ochraceus* 11 alpha hydroxylase with the top 10 BLAST hits from GenBank

5	CAA75565	1	---MANHSSSSYHEFYKDHSTVL	LMSEKPVILPSLILGTCAVLLCIQWLK--	POPLIM				
	CAB91316	1	-----MERLDIKST	DPSATPFSYLVTAFLLAVVV	SLQGPRF-PKNIKH				
	CAB56503	1	-----LLFCFILSKTTKK	GQNSQYS-NHDELP					
	AAB94588	1	-----MVMEHNNHTPF	SIYFITSILFIFFVFVKLVORS--	DSKTS-STCKLP				
	pMON45624	1	-----MPFFTGLLAIYHS	LILDNPVQTLSTIVVLAAY--LATLQ--	PSDLPE				
10	CAA75566	1	-----MSIFNMITSYAGS	QLLPFYIAIFVFTLVPAIR	SWLELRK-GSVVPL				
	AAD34552	1	---MTVDALTQPHHLLSLAWNDT	QQHGSWFAPLVTT	SAGLLCLLL-LCSSGR--	RSDLPV			
	CAA75567	1							
	CAA76703	1	MSKSNMNSTSHETLF	QQLVLGLDRMPLMDVHWLIYVAF	GAWLCS-VIHLVSSSSTVKVP				
	CAA57874	1							
CAA91268	1	-----MALLIL	SLVISIFTFFIYIILARRER	EKLREKIGLSGPEPH					
15									
	CAA75565	56	VNGRKFGELSNV	ARDTFGARQTEK	LKMSDPKPFITVGVGEH	PPKYAYEEN			
	CAB91316	45	LNPKGPLEFSDT	PKKEVVGSRQ	LANWFKANPNKPC	VVSTFGEALVPPRMANEEN			
	CAB56503	28	PGPPQIPILGNA	QLSGGH-TH	ILRDIAKKYGPLMHL	-IGVSTVASSPQIAEEIFR			
	AAB94588	45	PGPRTLPLIGNI	QIVGSLPVHY	YKNLADKYGPLMHL	-IGVSNIVTSPEMAQEMK			
20	pMON45624	46	LNPAPKPFETNR	RVHEFVENS	SEARRELGHEPY	LMVSGSLVLPPECADEEN			
	CAA75566	48	ANPPD-SLFGTGT	TERSEVKLS	EEAKERSLFPNEPF	LLTWGEVLPDFADEEN			
	AAD34552	56	FNEKTWWELT	TMAARD	DANAPSWESWFSQ	N-DKPIEFIVSGYCTLPSSMADEPK			
	CAA75567	1							
	CAA76703	61	VVGYSVFEPTWLL	LRVWEGGS	GOYNKFKDSIFQVRKL	GTDVPPNYIDEVKK			
25	CAA57874	1							
	CAA91268	43	WFLGNLQTAER	EELGDDAN	WFNELHEQYGETFGIY	-YGSQMNVSNEKDIKEVFI			
30									
	CAA75565	116	NEK	STMAA--FKW	FYAHLPGFEG--FREGTNE	SIEKLVARHQLT--QITLTGA			
	CAB91316	105	DDR	STRWT--YKA	FHLPGFEG--FGEASRES	IIOEVIMRDLT--NYENKYTEPLA			
	CAB56503	86	THD	LADRP	SNLESEFIVSYDESDMV	SPYGNWQREKSMELL	SOSSQSFRSIRE		
	AAB94588	104	THD	NSDRP--DFV	LSRIVSYNGSGIVFSQHGDY	WQREACTVELLTARVQSFRSIRE			
35	pMON45624	106	DPR	DEETPT--TDDS	GYIPGFDA----LN-ADPN	TVVTKYLT--RANKTAPIS			
	CAA75566	107	DPR	SESKAA--MQDN	AGIPGFET--VALVGREDQLQ	VARKQLT--THESAVIEPIS			
	AAD34552	115	MKE	CMYKFLG--TDF	SHLPGFDG--FKEVTRDA	LITVVMNQFO--TQAPKYVKPLA			
	CAA75567	1							
	CAA76703	121	LS	----	QDKTRSVEPFINDFA	QYQT--RGMVFLQSDLQ	NVIQQLT--PKVVS		
40	CAA57874	1							
	CAA91268	102	KNFSN	SDRS--VPS	IYEANQLTASLLMNSYSSGW	HTRSAIAPIS--TGKKAQETEN			
45									
	CAA75565	170	BE	CALVKDYTDSP--	WHD	TAKDANKL	ARITSRVFGKECN	NPWLR--STYA	
	CAB91316	159	QETS	MAEANL	PKAANGWST	NRSKLP	VARISRYTGEE	CRNEFWLKYI-QQYT	
	CAB56503	146	BE	VLNFKS	EG---SKEG	TRN	SKE	SLLYGITTAAAFGEKNKNT	EPRLDQLTK
	AAB94588	163	BE	VAEL	VKKHAATASEEGGS	IFNTQS	YSMTFG	AARAAFGKKSRYQ	OVESNMHKQLM
50	pMON45624	156	HE	ASIA	KAMLGDDP--	WRE	YPARD	LOL	VARISRYTGEE
	CAA75566	161	RE	STLA	SLNFGETT--	WRA	RKPA	LD	ARISRYLGDQ
	AAD34552	169	NE	ASGI	TD	FGDSN--	WHT	P	YNQCDL
	CAA75567	17	MKT	SFR	WPRTS----	KSS	SYDM	ERTVAL	SGRAVGLP
	CAA76703	173	BE	LDYA	TKEMPDMKND	WVE	DS	SI	YRL
55	CAA57874	1							
	CAA91268	159	SK	VDLF	DI	REKAS--	SGQKWD	YDDFQGL	PLD
60									
	CAA75565	227	VI	AFRAVEE	L	REP--SWLR	P	QW	FPHCTQS
	CAB91316	218	LD	GFGAAED	L	REP--AALR	P	YHW	F
	CAB56503	202	AV	AEPNIAD	F	PSL-KFLQL	STSKYKIEKIH	QFDVIVETI	KGHKE
	AAB94588	223	LG	GFSVAD	P	SS--R	FOM	GATG-KLEKVH	RVTD
65	pMON45624	213	AL	AFGVGDK	L	REP--R	REP	YHWF	PSCWE
	CAA75566	218	TN	FYTASTN	L	RMPP--RS	R	PLAHWF	PECRK
	AAD34552	226	VT	MAIQARQ	L	REP--V	L	RPI	HWLE
	CAA75567	70	QC	VSIRDQ	L	ETAS--P	YLRP	IGPE	PSVRSVRH
	CAA76703	232	ES	LITGFI	L	RAVE--H	L	RPE	IAPL
65	CAA57874	1							
	CAA91268	217	K	ITINNFTY	F	HSSSPGTFHF	EST	QIHT	TG

THE UNIVERSITY OF CHICAGO

Figure 5 - Phylogenetic tree showing the relatedness of *Aspergillus ochraceus* 11 α hydroxylase to the top 10 BLAST hits from GenBank



**Figure 6 – Percent homology of *Aspergillus ochraceus* 11
alpha hydroxylase to the top 10 BLAST hits from GenBank**

Accession Number	Species	% ID to 11a OH
CAB91316	<i>Neurospora crassa</i>	40
CAA76565	<i>Gibberella fujikuroi</i>	37
CAA75566	<i>Gibberella fujikuroi</i>	37
AAD34552	<i>Aspergillus terreus</i>	29
CAA75567	<i>Gibberella fujikuroi</i>	24
CAA57874	<i>Fusarium oxysporum</i>	24
CAA76703	<i>Gibberella fujikuroi</i>	23
CAB56503	<i>Catharanthus roseus</i>	14
AAB94588	<i>Glycine max</i>	14
CAA91268	<i>Caenorhabditis elegans</i>	12

Figure 7 – Amino acid homology alignment of *A. ochraceus* and human oxidoreductase to NADPH cytochrome P450 reductases from *A. niger*, mouse, and *S. cerevisiae*

5	PMON45605	1	MGDSHYDTSSIVSEAVAEVSLFSITDMILFSLIVGLTYWFLFRKKKEEVPFEFKIOTL
	human	1	MGDSHYDTSSIVSEAVAEVSLFSITDMILFSLIVGLTYWFLFRKKKEEVPFEFKIOTL
	mouse	1	MGDSHEDTSATVPEAVAEVSLFSTTDMLFSLIVGLTYWFLFRKKKEEVPFEFKIOTL
	pMON45632	1	--MAQLDITLLVLVALLVGSAYFTKG-----TYWAKADPYA--SAGPAMNGG
	niger	1	--MAQLDITLLVLVALLVGSAYFTKG-----TYWAKAKTTPMP--LPAPKRMNGA
10	yeast	1	--MPFGIDNIDFTVLDAGLVAVLLYVKRN-----SIKELIIMSDDG-----DIT--
	PMON45605	61	TSSVRESSEFVEKMKKTGKNIIVFYGSQTGTAEETANRLSKD-AHRYGMRGMSADPEEYDL
	human	61	TSSVRESSEFVEKMKKTGKNIIVFYGSQTGTAEETANRLSKD-AHRYGMRGMSADPEEYDL
	mouse	61	APPVKESSEFVEKMKKTGKNIIVFYGSQTGTAEETANRLSKD-AHRYGMRGMSADPEEYDL
	pMON45632	47	AKAGKTRDIVKMDETGNCVIFYGSQTGTAEVYASRLAKEGSORFCEKTMVADLLEYDY
15	niger	47	AKAGKTRNITEKMEETGNCVIFYGSQTGTAEVYASRLAKEGSORFCEKTMVADLLEYDY
	yeast	42	AVSGNRDIAIVTENNANYLVLYASQTGTAEVYAKKFSKELVAKINLVWCADVENYDF
	PMON45605	120	ADLSSLPEIDNALVVFCMATYGECDPTDNAQDFYDLQ-----ET-----DVDLSGMYKE
	human	120	ADLSSLPEIDNALVVFCMATYGECDPTDNAQDFYDLQ-----ET-----DVDLSGMYKE
	mouse	120	ADLSSLPEIDKSLVVFCMATYGECDPTDNAQDFYDLQ-----ET-----DVDLIGMYKE
20	pMON45632	107	ENLEKFPEDK-VVFFVILATYGECDPTDNAVFYQFVTGEDAAFEAGATADKPLSSLYKY
	niger	107	ENLDQFPEDK-VAFFVILATYGECDPTDNAVFYQFVTGEDDVAFES-ASADEKPLSKLYKY
	yeast	102	ESLNDYFV----VVSIFISTYGECDPTGAVNFEDETCN----AEAG-----ALSNRY
	PMON45605	169	AVFGLGNKTYEHFNAMGKYVDKRLQELGAQRIFELGLGDD-DGNLEEDFTITWREQFWPAV
	human	169	AVFGLGNKTYEHFNAMGKYVDKRLQELGAQRIFELGLGDD-DGNLEEDFTITWREQFWPAV
30	mouse	169	AVFGLGNKTYEHFNAMGKYVDKRLQELGAQRIFELGLGDD-DGNLEEDFTITWREQFWPAV
	pMON45632	165	VTPLGNNTYEHFNAMVNVDAALTKFGAQRIGSAGEGDDGAGTMEEDFLAKKEPMMAL
	niger	164	VAFGLGNNTYEHFNAMVNVDAALTKFGAQRIGSAGEGDDGAGTMEEDFLAKKEPMMAL
	yeast	148	NMFGLGNSTYEFENCAAKKAKELSAAGAIRGKLGAEADDGAGTTEDYMAKESILEVL
35	PMON45605	228	CEHFGVEATGEESSIROQYELVVHTD----DAKVYVNGEMGRKLSY-----ENQKP
	human	228	CEHFGVEATGEESSIROQYELVVHTD----DAKVYVNGEMGRKLSY-----ENQKP
	mouse	228	CEHFGVEATGEESSIROQYELVVHTD----MDIAKVYVNGEMGRKLSY-----ENQKP
	pMON45632	225	SEAMNLC---ERDAYEPVFNVTEDSLSPDENVYLGEPTQGLQ-----GEPKG
	niger	224	SESMDFE---EREAVYEPVFCVTENESLSPDETIVYLGEPTQSHLQ-----GTPKG
40	yeast	208	KDELHL---EPEAKFTSDFQYTVLN---EITDSLSLGEPSAHYLPASHQLNRNADGIQLG
	PMON45605	275	PFDANKPFLAAYTTNRKLNQGTERRHLMHLELDISDSKIRYESGDHVAVVPANDSALVNOL
	human	275	PFDANKPFLAAYTTNRKLNQGTERRHLMHLELDISDSKIRYESGDHVAVVPANDSALVNOL
	mouse	275	PFDANKPFLAAYTTNRKLNQGTERRHLMHLELDISDSKIRYESGDHVAVVPANDSLVNOL
	pMON45632	273	PESAHPFLAPAESRELFVVKORNCHEHLESIAGSNISYQIGDHTAVVPTNAGSEVRE
45	niger	272	PESAHPFLAPAESRELFVVKORNCHEHLESIAGSNISYQIGDHTAVVPTNAGSEVRE
	yeast	262	PFLLSQPVYAPVKSRELFSSNRNCHEHLESIAGSNISYQIGDHLAVVPSNPLEKVEQF
50	PMON45605	335	GKILGAD--LDVVMSTNNLDEESNKKHPPFCPTSYRTALTYYLEITNPPTNVLYELAOY
	human	335	GKILGAD--LDVVMSTNNLDEESNKKHPPFCPTSYRTALTYYLEITNPPTNVLYELAOY
	mouse	335	GEILGAD--LDVVMSTNNLDEESNKKHPPFCPTTYRTALTYYLEITNPPTNVLYELAOY
	pMON45632	333	LQAFGLGKRHSVINKGLD--VTAKVPIPTPTTYDAAMRYLYEVCAPVSRQFVSTLAAE
	niger	332	LQAFGLGKRHSVINKGLD--VTAKVPIPTPTTYDAAMRYLYEVCAPVSRQFVATLAAE
55	yeast	322	LSIFNLD--PETTFDLKPLD--PTVKVPPFETPTTIGAAIKHYLEITGCVSRQFSSLIQF
	PMON45605	393	AS-EPSEQELLRKMASSSGEGKELYLSWVVEARRHILAILQDCP--SLRPPIDHLCCELLPR
	human	393	AS-EPSEQELLRKMASSSGEGKELYLSWVVEARRHILAILQDCP--SLRPPIDHLCCELLPR
	mouse	393	AS-EPSEQEHLRKMASSSGEGKELYLSWVVEARRHILAILQDYP--SLRPPIDHLCCELLPR
	pMON45632	391	APDEAKAEVRLGDKDYFHEKTNRCFNIAQ--ALQSTSKP-FTAVFSSLIEGTTK
60	niger	390	APMRKARORICVWVQAQ-LFPFEGHQPMQHAQ--ALQSTSKP-FSAVFFSSLIEGTTK
	yeast	378	APNADVKKKTLLSKDKDQFVVEITSKCFNIAD--ALKYLSGAKWDNVEMQFLVESMFO
65	PMON45605	451	LQARYYSIASSSKVHPNSVHICAVVVEYETK----AGRINKGVATNWLRAKEP--AGE--
	human	451	LQARYYSIASSSKVHPNSVHICAVVVEYETK----AGRINKGVATNWLRAKEP--AGE--
	mouse	451	LQARYYSIASSSKVHPNSVHICAVAVEYBAK----SGRANKGVATSWLRTKEP--AGE--
	pMON45632	448	LQPRYYISSSSSLVQKKESITAVVESVRLP---GEEIVKGVITNLLALKKQNGRSL
	niger	446	LQPRYYISSSSSLVQKKESITAVVESVRLP---GASIVKGVITNLLALKKQNGRSL
70	yeast	436	QTPRYYSISSSSLSKQVHVTSEVENPNPELP-DAPPGVGVITNLLRNILACNNVNI

5 PMON45605 503 -----NGGR-----ALVPMFVRKSFRLPFKATTPVIMVGP GTGVAPFI GFTIQE
human 503 -----NGGR-----ALVPMFVRKSFRLPFKATTPVIMVGP GTGVAPFI GFTIQE
mouse 503 -----NGGR-----ALVPMFVRKSFRLPFKATTPVIMVGP GTGVAPFI GFTIQE
pMON45632 505 PDPHG--TYSITGPRNKYDGIHVPVHVRSNFKLPSDPSRPVIMVGP GTGVAPFRGF IQE
niger 503 SRPSR-LDLLHGP RNKYDGIHVPVHVRSNFKLPSDPSRPVIMVGP GTGVAPFRGF IQE
yeast 495 AETNLPVHYDLNGPRKLANYKLPVHVRSNFKLPSNPSPTVIMVGP GTGVAPFRGF IQE

10 PMON45605 547 RAWLRQ---QCKE---VGETLLYGCRRSDEDELYREELAQFHED-GALTQLNVAFSRE-
human 547 RAWLRQ---QCKE---VGETLLYGCRRSDEDELYREELAQFHED-GALTQLNVAFSRE-
mouse 547 RAWLRQ---QCKE---VGETLLYGCRRSDEDELYREELAQFHED-GALTQLNVAFSRE-
pMON45632 564 RAALAA---KCEK---VGETLLYGCRRSDEDELYREELAQFHED-GALTQLNVAFSRE-
niger 562 RAALAA---KCEK---VGETLLYGCRRSDEDELYREELAQFHED-GALTQLNVAFSRE-
yeast 555 RVAFLESQKRCGNNVSLGKHILFYGSRNQD-DELYQDEWPEYAKKLDSEFEMVVAHSRLP

15 PMON45605 599 QSHKVYVQHLLKQDEEHWKLI-EGGAHIYVCGDARNMARDVQNTFYDIVAELCAMEHAQ
human 599 QSHKVYVQHLLKQDEEHWKLI-EGGAHIYVCGDARNMARDVQNTFYDIVAELCAMEHAQ
mouse 599 QSHKVYVQHLLKQDEEHWKLI-EGGAHIYVCGDARNMARDVQNTFYDIVAELCAMEHAQ
pMON45632 617 SAEKVYVQHLLKQDEEHWKLI-EGGAHIYVCGDARNMARDVQNTFYDIVAELCAMEHAQ
niger 615 GPQKVYVQHLLKQDEEHWKLI-EGGAHIYVCGDARNMARDVQNTFYDIVAELCAMEHAQ
yeast 614 NTKKVYVQDKLKDYEDQVEEMI-NNGAFTYVCGDAKGMARGVSTALVGLSRGKSHITTE

20 PMON45605 599 QSHKVYVQHLLKQDEEHWKLI-EGGAHIYVCGDARNMARDVQNTFYDIVAELCAMEHAQ
human 599 QSHKVYVQHLLKQDEEHWKLI-EGGAHIYVCGDARNMARDVQNTFYDIVAELCAMEHAQ
mouse 599 QSHKVYVQHLLKQDEEHWKLI-EGGAHIYVCGDARNMARDVQNTFYDIVAELCAMEHAQ
pMON45632 617 SAEKVYVQHLLKQDEEHWKLI-EGGAHIYVCGDARNMARDVQNTFYDIVAELCAMEHAQ
niger 615 GPQKVYVQHLLKQDEEHWKLI-EGGAHIYVCGDARNMARDVQNTFYDIVAELCAMEHAQ
yeast 614 NTKKVYVQDKLKDYEDQVEEMI-NNGAFTYVCGDAKGMARGVSTALVGLSRGKSHITTE

25 PMON45605 658 AVDYKKLMTKGRYSLDVWS
human 658 AVDYKKLMTKGRYSLDVWS
mouse 659 AVDYKKLMTKGRYSLDVWS
pMON45632 676 GEEMMKHMRSGSYQDDVWS
niger 674 GEEMMKHMRSGSYQDDVWS
yeast 673 ATTELKMLKTSGRYQEDVW-

30 PMON45605 658 AVDYKKLMTKGRYSLDVWS
human 658 AVDYKKLMTKGRYSLDVWS
mouse 659 AVDYKKLMTKGRYSLDVWS
pMON45632 676 GEEMMKHMRSGSYQDDVWS
niger 674 GEEMMKHMRSGSYQDDVWS
yeast 673 ATTELKMLKTSGRYQEDVW-

35 PMON45605 (SEQ ID NO: 03)
human (SEQ ID NO: 06)
mouse (SEQ ID NO: 39)
pMON45632 (SEQ ID NO: 05)
niger (SEQ ID NO: 38)
yeast (SEQ ID NO: 37)

Figure 8 – Amino acid homology alignment of *A. ochraceus* oxidoreductase to NADPH cytochrome P450 reductases from *A. niger* and *S. cerevisiae*

5	A.niger	1	MAQLDTLDLVVLA VLLVGSVAYFTKGT YWAVAKERMPLPAPRMNGAAKAGKTRNITIKM
	A.ochraceus	1	MAQLDTLDLVVLA VLLVGSVAYFTKGT YWAVAKDPYASAPAMNGCAKAGKTRDIVOKM
	S.cerevisiae	1	MPFGDNTDFTVLAGLVAVLVYKENSKEELMSDDSDITAVSSG-----NRDIAQVV
10	A.niger	60	ETGKNCVIFYGSQTGAEDYASRLAKEGSORFGLKTMVADLEEDYDENLDOFPEDKVAE
	A.ochraceus	60	ETGKNCVIFYGSQTGAEDYASRLAKEGSORFGLKTMVADLEEDYDENLEKFPEDKVVE
	S.cerevisiae	55	TENNKNYLVLYASQTGAEDYAKKFSKELVAKENLNVMCADENYDEESNDVPE--VVS
15	A.niger	120	FVLATYGEGETDNAVIFYOFETGDDVAFES-ASADEKPLSKLKYYVAFGLGNNTYEHYNA
	A.ochraceus	120	FVLATYGEGETDNAVIFYOFETGDDAFAESGAADEKPLSSLYVTFCGLGNNTYEHYNA
	S.cerevisiae	113	IFISTYGEGETFDGAVNFEDFIC-----NAAGALSNLYNMFGLGNSTYEFENG
20	A.niger	179	MVRQVDAAFQRLGPORIGSAGEGDDGAGTMEEDFLAWKEPMWAALSESMDLEEREAVYEP
	A.ochraceus	180	MVRNVDAALKFGAORIGSAGEGDDGAGTMEEDFLAWKEPMWAALSEAMNLOERNAVYEP
	S.cerevisiae	163	AAAKAKKHLAAGATKCKLGEADDGAGTDEDYMAWKESLLEVLKDEPHLDEQAKETS
25	A.niger	239	VFCVTENESLSPEDENVYLGEPTQSHLC-----GTPKGPYSAHNPFIAPAESREL
	A.ochraceus	240	VFCVTENESLSPEDENVYLGEPTQSHLC-----GTPKGPYSAHNPFIAPISEREL
	S.cerevisiae	223	QEQYT---VLEITDSLSLGEPSAHYLP SHQLNRNADGQLGPEDLSPFIAPIVKSRREL
30	A.niger	290	FIVKDRNCLHMEISTAGSNLYOTGDHIAVWPTNAGAEVDRFLQAFGLGKRSVINKG
	A.ochraceus	291	FIVKDRNCLHMEISTAGSNLYOTGDHIAVWPTNAGSEVDRFLQAFGLGKRSVINKG
	S.cerevisiae	280	FSSNDRCNTHSEFDLSGSNLYKYSTGDHIAVWPTNPLEKVEQFLSIFNLPE--EITFDKRP
35	A.niger	350	IDVTAKVPIPTPTTYDAVRYYLEVCAPVSRQFVSTLAAPMRKAEQRLCQVWVQOG-LF
	A.ochraceus	351	IDVTAKVPIPTPTTYDAVRYYLEVCAPVSRQFVSTLAAPMRKAEQRLCQVWVQOG-LF
	S.cerevisiae	338	LDPTVIVPFPPTPTTIGAAITHYLEETGPVSRQFLSSLIQFAPNADVKEPILITLSKDKDOF
40	A.niger	409	PREGHQPMLOHAQALQSITS-KPFSAVPFSLLEGITKLQPRYYSISSSSLVQDKISIT
	A.ochraceus	411	HEKITNRCFNIAQALQSITS-KPFSAVPFSLLEGITKLQPRYYSISSSSLVQDKISIT
	S.cerevisiae	398	AVEITISKYFNIAADALKYSDGAKMDNVPMQFLVESVPOITPRYYSISSSSLSKQTVHVT
45	A.niger	468	AVVESVRLP--GASHNVKGVTTNYLLALAKKONGRS-SRFSR-LDLLHHGPRNKYDGIHV
	A.ochraceus	470	AVVESVRLP--GASHNVKGVTTNYLLALAKKONGEPPSPDHG-LTYSITGPRNKYDGIHV
	S.cerevisiae	458	SVENFPNPELPEAPPGVGVTTNLLRNQLAONNVNIAATNLPMHYDNGPRKLANYE
50	A.niger	525	PVHVRHSNFKLPSPDSRPIMVGPCTGVAPFRGFIQERAALAAGKER-----VGPTMLF
	A.ochraceus	527	PVHVRHSNFKLPSPDSRPIMVGPCTGVAPFRGFIQERAALAAGKER-----VGPTMLF
	S.cerevisiae	518	PVHVRHSNFKLPSPDPSTPVIMIGPGTGVPFRGFIRERVAFLSQKKGNNVSGKHMLF
55	A.niger	579	FGCRKSDDEFLYKDEWKTYQQLGDNLKIIITAFSRE-GPQKVYVQHRLREHSELVSDLLK
	A.ochraceus	581	FGCRKSDDEFLYKDEWKTYQQLGDSLKIIITAFSRE-SAEKVYVQHRLREHSELVSDLLK
	S.cerevisiae	578	YGSRNED-DRLYQDEWPEYAKKLDGSFEEVVAHSRLPNTKKVYVQDLKDYEQVFEMEN
60	A.niger	638	QKATFYVCGDAANMAREVNVLVLGQIIAQRGLPAEKGEEMVKHMRRRGRYQEDVWS
	A.ochraceus	640	QKATFYVCGDAANMAREVNVLVLGQIIAQRGLPAEKGEEMVKHMRSSGQYQEDVWS
	S.cerevisiae	637	NGAFIYVCGDAKGMAGVSTALVGLISRGISTTTEATEELKMLKSGRYQEDVW-

A.ochraceus, PMON45632 (SEQ ID NO: 05)
A.niger (SEQ ID NO: 38)
S.cerevisiae, yeast (SEQ ID NO: 37)

Figure 9 – Phylogenetic tree showing the relatedness of *Aspergillus ochraceus* and human oxidoreductase to reductases from *A. niger*, yeast, and mouse.

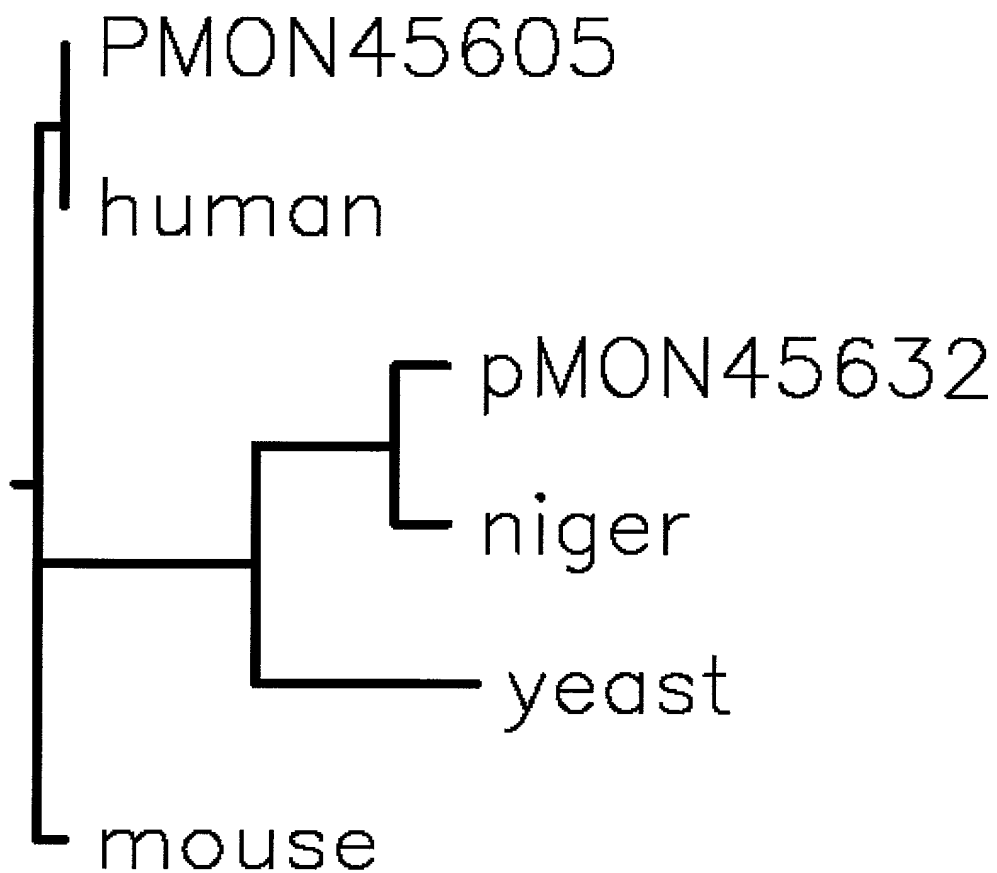


Figure 10 – Percent homology between *Aspergillus ochraceus* oxidoreductase to reductases from *A. niger*, yeast, and mouse and human.

Accession number	organism	% id to A.och oxred
CAA81550	<i>A. niger</i>	84
BAA02936	<i>S. cerevisiae</i>	37
BAA04496	mouse	34
AAB21814	human	33

[illegible]

Figure 11 – Amino acid homology alignment of human oxidoreductase with the top 4 hits from SwissProt

5	PMON45605	1	MGDSHVDTSSTVSEAVAAEEVSLFSMTDMFLFSLIVGLLTYWFFRKKKEEVPEFKIOTL
	human	1	MGDSHVDTSSTVSEAVAAEEVSLFSMTDMFLFSLIVGLLTYWFFRKKKEEVPEFKIOTL
	rabbit	1	MGDSHVDTSSTVSEAVAAEEVSLFSMTDMFLFSLIVGLLTYWFFRKKKEEVPEFKIOTL
	rat	1	MGDSHVDTSSTVSEAVAAEEVSLFSMTDMFLFSLIVGLLTYWFFRKKKEEVPEFKIOTL
	mouse	1	MGDSHVDTSSTVSEAVAAEEVSLFSMTDMFLFSLIVGLLTYWFFRKKKEEVPEFKIOTL
10	pig	1	MGDSHVDTSSTVSEAVAAEEVSLFSMTDMFLFSLIVGLLTYWFFRKKKEEVPEFKIOTL
	PMON45605	61	TSSVKESSFVEKMKKTGRNIVFYGSQTGTAEFANRLSKDAHRYGMRGMSADPEEYDL
	human	61	TSSVKESSFVEKMKKTGRNIVFYGSQTGTAEFANRLSKDAHRYGMRGMSADPEEYDL
	rabbit	61	TSSVKESSFVEKMKKTGRNIVFYGSQTGTAEFANRLSKDAHRYGMRGMSADPEEYDL
	rat	61	APPVKESSFVEKMKKTGRNIVFYGSQTGTAEFANRLSKDAHRYGMRGMSADPEEYDL
15	mouse	61	APPVKESSFVEKMKKTGRNIVFYGSQTGTAEFANRLSKDAHRYGMRGMSADPEEYDL
	pig	61	TSSVKESSFVEKMKKTGRNIVFYGSQTGTAEFANRLSKDAHRYGMRGMSADPEEYDL
20	PMON45605	120	ADLSSLPEIDNALVVFECMATYGECDPTDNAQDFYDWLQETDVLGVKFAVFLGNKTYE
	human	120	ADLSSLPEIDNALVVFECMATYGECDPTDNAQDFYDWLQETDVLGVKFAVFLGNKTYE
	rabbit	121	ADLSSLPEIDNALVVFECMATYGECDPTDNAQDFYDWLQETDVLGVKFAVFLGNKTYE
	rat	120	ADLSSLPEIDNALVVFECMATYGECDPTDNAQDFYDWLQETDVLGVKFAVFLGNKTYE
	mouse	120	ADLSSLPEIDNALVVFECMATYGECDPTDNAQDFYDWLQETDVLGVKFAVFLGNKTYE
25	pig	120	ADLSSLPEIDNALVVFECMATYGECDPTDNAQDFYDWLQETDVLGVKFAVFLGNKTYE
	PMON45605	180	HFNAMGKYVDKRLLEQLGAORIFELGLGDDGDNLEEDFITWREQFWPAVCEHFGVEATGEE
	human	180	HFNAMGKYVDKRLLEQLGAORIFELGLGDDGDNLEEDFITWREQFWPAVCEHFGVEATGEE
	rabbit	181	HFNAMGKYVDKRLLEQLGAORIFELGLGDDGDNLEEDFITWREQFWPAVCEHFGVEATGEE
	rat	180	HFNAMGKYVDKRLLEQLGAORIFELGLGDDGDNLEEDFITWREQFWPAVCEHFGVEATGEE
30	mouse	180	HFNAMGKYVDKRLLEQLGAORIFELGLGDDGDNLEEDFITWREQFWPAVCEHFGVEATGEE
	pig	180	HFNAMGKYVDKRLLEQLGAORIFELGLGDDGDNLEEDFITWREQFWPAVCEHFGVEATGEE
35	PMON45605	240	SSIROYELVVHTDIDAKVYMGEMGRKLSYENOKPPFDAKNPFLAAVTNKRKLNOGTERH
	human	240	SSIROYELVVHTDIDAKVYMGEMGRKLSYENOKPPFDAKNPFLAAVTNKRKLNOGTERH
	rabbit	241	SSIROYELVVHTDIDAKVYMGEMGRKLSYENOKPPFDAKNPFLAAVTNKRKLNOGTERH
	rat	240	SSIROYELVVHTDIDAKVYMGEMGRKLSYENOKPPFDAKNPFLAAVTNKRKLNOGTERH
	mouse	240	SSIROYELVVHTDIDAKVYMGEMGRKLSYENOKPPFDAKNPFLAAVTNKRKLNOGTERH
40	pig	240	SSIROYELVVHTDIDAKVYMGEMGRKLSYENOKPPFDAKNPFLAAVTNKRKLNOGTERH
	PMON45605	300	LMHLELDISDSKIRYESGDHVAVYPANDSALVNOLGELGADLDVVMISLNNLDEESNKKH
	human	300	LMHLELDISDSKIRYESGDHVAVYPANDSALVNOLGELGADLDVVMISLNNLDEESNKKH
	rabbit	301	LMHLELDISDSKIRYESGDHVAVYPANDSALVNOLGELGADLDVVMISLNNLDEESNKKH
	rat	300	LMHLELDISDSKIRYESGDHVAVYPANDSALVNOLGELGADLDVVMISLNNLDEESNKKH
45	mouse	300	LMHLELDISDSKIRYESGDHVAVYPANDSALVNOLGELGADLDVVMISLNNLDEESNKKH
	pig	300	LMHLELDISDSKIRYESGDHVAVYPANDSALVNOLGELGADLDVVMISLNNLDEESNKKH
50	PMON45605	360	FPFCPTSYRTALTYLDITNPPRTNVLYELAQYASEPSEQELRKMASSSGEGKELYLSW
	human	360	FPFCPTSYRTALTYLDITNPPRTNVLYELAQYASEPSEQELRKMASSSGEGKELYLSW
	rabbit	361	FPFCPTSYRTALTYLDITNPPRTNVLYELAQYASEPSEQELRKMASSSGEGKELYLSW
	rat	360	FPFCPTSYRTALTYLDITNPPRTNVLYELAQYASEPSEQELRKMASSSGEGKELYLSW
	mouse	360	FPFCPTSYRTALTYLDITNPPRTNVLYELAQYASEPSEQELRKMASSSGEGKELYLSW

mouse 360 PFPCPTVVRTALTYYLDTNPPRTNVLYELAQYASEPSEQHLKMASSSGEGKELYLSW
pig 360 PFPCPTVVRTALTYYLDTNPPRTNVLYELAQYASEPSEQOLRMASSSGEGKELYLSW

5 PMON45605 420 VVEARRHILAILQDCPSLRPPIDHLCCELLPRLOARYYSSASSKVPNSVHICAVVVEYE
human 420 VVEARRHILAILQDCPSLRPPIDHLCCELLPRLOARYYSSASSKVPNSVHICAVVVEYE
rabbit 421 VVEARRHILAILQDYPSLRPPIDHLCCELLPRLOARYYSSASSKVPNSVHICAVVVEYE
rat 420 VVEARRHILAILQDYPSLRPPIDHLCCELLPRLOARYYSSASSKVPNSVHICAVVVEYE
mouse 420 VVEARRHILAILQDYPSLRPPIDHLCCELLPRLOARYYSSASSKVPNSVHICAVVVEYE
10 pig 420 VVEARRHILAILQDYPSLRPPIDHLCERLPRLOARYYSSASSKVPNSVHICAVVVEYE

15 PMON45605 480 TKAAGRINKGVATNWLRAKEPAGENGGRALVPMFVRKSQFRLPFKATTPVIMVGPCTGVAP
human 480 TKAAGRINKGVATNWLRAKEPAGENGGRALVPMFVRKSQFRLPFKATTPVIMVGPCTGVAP
rabbit 481 TKAAGRINKGVATSWLRAKEPAGENGGRALVPMFVRKSQFRLPFKATTPVIMVGPCTGVAP
rat 480 AKSGRVNKGVATSWLRAKEPAGENGGRALVPMFVRKSQFRLPFKATTPVIMVGPCTGVAP
mouse 480 AKSGRVNKGVATSWLRTKEPAGENGGRALVPMFVRKSQFRLPFKATTPVIMVGPCTGVAP
pig 480 TKSGRVNKGVATSWLRAKEPAGENGGRALVPMFVRKSQFRLPFKATTPVIMVGPCTGVAP

PMON45605 540 FIGFIQERAWLRQOGKEVGETLLYYGCRSDEDYLYREELAQFHHKDGALTQLNVAFSREQ

human 540 FIGFIQERAWLRQOGKEVGETLLYYGCRSDEDYLYREELAQFHHKDGALTQLNVAFSREQ

rabbit 541 FIGFIQERAWLRQOGKEVGETLLYYGCRRAEDYLYREELAGFQKDGTLSQLNVAFSREQ

rat 540 FIGFIQERAWLRQOGKEVGETLLYYGCRSDEDYLYREELARFHKDGALTQLNVAFSREQ

5 mouse 540 FIGFIQERAWLRQOGKEVGETLLYYGCRSDEDYLYREELARFHKDGALTQLNVAFSREQ

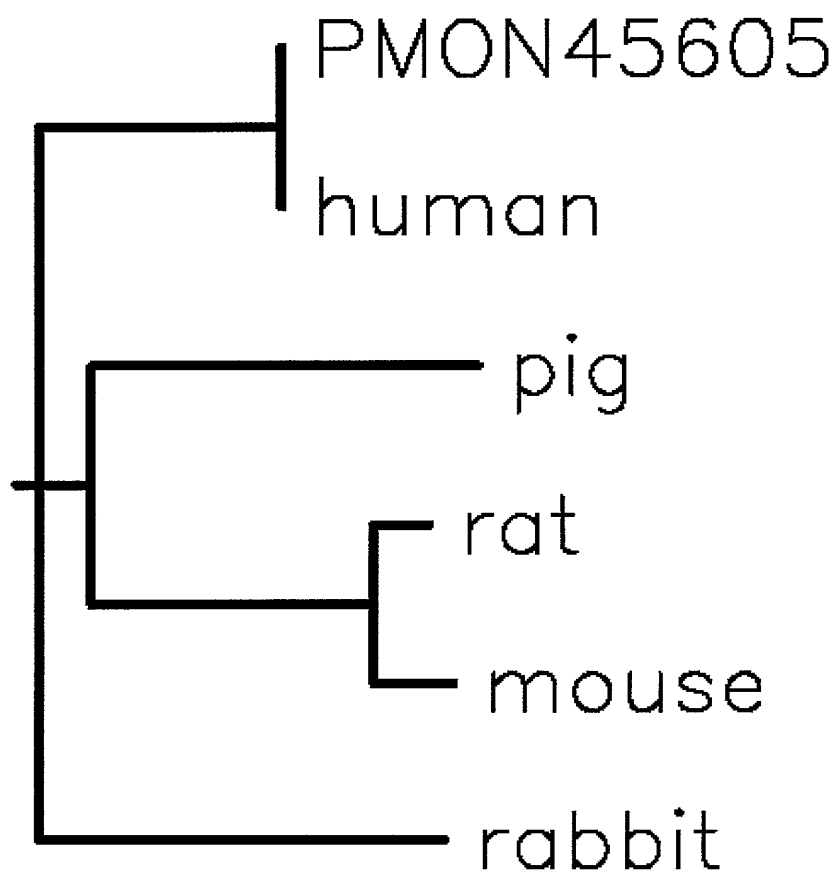
pig 540 FIGFIQERAWLRQOGKEVGETLLYYGCRSDEDYLYREELAQFHHKAGALTRLSVAFSREQ

10

PMON45605	600	SHKVVYVQHLLKQDEHLWLKLI	EGGAHIYVCGDARNMARDVQNTFFYDIAVELGAM EH AOA
human	600	SHKVVYVQHLLKQDEHLWLKLI	EGGAHIYVCGDARNMARDVQNTFFYDIAVELGAM EH AOA
rabbit	601	AQKVVYVQHLLRDRDEHLWLFL	IEHGGAHITVCGDARNMARDVQNTFFYDIAVELGAM EH AOA
rat	600	AHKVVYVQHLLKRDRDEHLWLKLI	HEGGAHIYVCGDARNMAKDVQNTFFYDIAVEFQ PM PF ET OA
mouse	600	AHKVVYVQHLLKRDEHLWLKLI	HEGGAHIYVCGDARNMARDVQNTFFYDIAVEFQ PM PF ET OA
pig	600	PQKVVYVQHLLKRDEHLWLKLI	HEGGAHIYVCGDARNMARDVQNTFFYDIAVEFQ PM PF ET OA

15				
	PMON45605	659	VDYVKKLMTKG RYSLDVWS	(SEQ ID NO: 03)
	human	659	VDYVKKLMTKG RYSLDVWS	(SEQ ID NO: 52)
	rabbit	661	VDYVKKLMTKG RYSLDVWS	(SEQ ID NO: 53)
20	rat	660	VDYVKKLMTKG RYSLDVWS	(SEQ ID NO: 54)
	mouse	660	VDYVKKLMTKG RYSLDVWS	(SEQ ID NO: 55)
	pig	660	VDYVKKLMTKG RYSLDVWS	(SEQ ID NO: 56)

Figure 12 – Phylogenetic tree showing the relatedness of human oxidoreductase (P16435) with top 4 hits from SwissProt



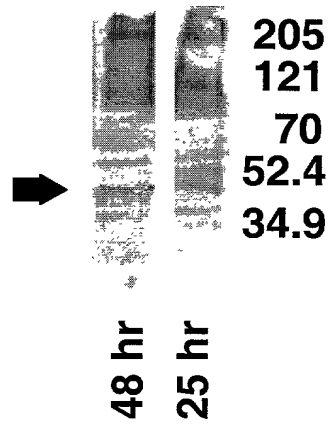
***Figure 13 – Percent homology between human oxidoreductase
and top 4 hits from SwissProt***

Accession number	Species	% id to human oxred
P00388	rat	92
P00389	rabbit	92
P37040	mouse	92
P04175	pig	91

Downloaded from www.sciencedirect.com

Figure 14 - Expression of *Aspergillus ochraceus* 11 α hydroxylase in transfected Sf9 insect cells

Expression of 11- α -Hydroxylase in Transfected Sf9 Cells



**Figure 15 - Expression of *Aspergillus ochraceus* P450
oxidoreductase in transfected Sf9 insect cells**

**Expression of Fungal P-450 Oxidoreductase
in Transfected Sf9 Cells**

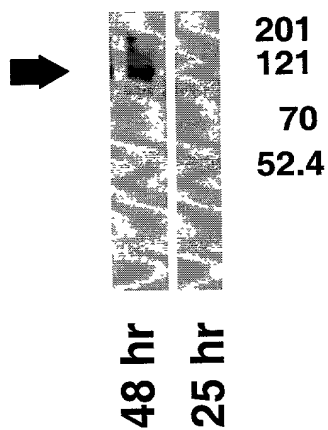


Figure 16 - Conversion of androstenedione to 11 alpha hydroxy androstenedione monitored by HPLC

